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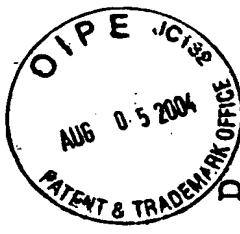


Axel ULLRICH et al.
DNA ENCODING MCK-10, A NOVEL
RECEPTOR TYROSINE
Atty. Dkt. No. 034536-0447
SN 09/551,188

1 CGGGCCTGAGACTGGGTGACTGGACCTAACAGAGAAATCCCTGAGGCTGGAGCCCCCACAG
61 CTGGCTTCGGAGCCGCTCCCGACACCCGAGCCCCGGCGGCCCTCCCCCTTCCGGCTCCTGGCT
121 CCGGCTCCTGGCTCTGGCTCCCTTCCGGCTCCTGGCTCTGGCTCCTGGCTCTGGCT
181 CCCGGGTCGGACGGCCTGGGTCTGGGTCAAGAGGGATGAGAGGATGAGAGGACTTGAAAGGAAT
241 TCACTGGCGATGGGGTTGGACTTGAAAGAGATGCCAACAGATGCTGCCAACCCCTTA

1 M G P E A L S S L L L L L L
301 GGCGGAGGGATCAGGGAGCTATGGGACCCAGGGCCCTGTCACTTACTGCTGCTGCTCT
15 V A S G D A D M K G H F D P A K C R Y A
361 TGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTGATCCTGCAAGTGCCTGGCTATG
35 L G M Q D R T I P D S D I S A S S W S
421 CCCTGGCCATGCAGGACCCAGACAGTGAATCCCAGAACGGACCATGCCGGACCAT
55 D S T A A R H S R L E S S D G D G A W C
481 CAGATTCCACTGCCGGCCACAGCAGGTGGAGAGGCAGTGAAGGGATGGCTCCAGGCTGGT
75 P A G S V F P K E E Y L Q V D L Q R L
541 GCCCGGAGGGTCGGTGTGGTCAAGGAGGGAGTACTTGCAAGGTGGATCTACAAAGGAC
95 H L V A L V G T Q G R H A G G L G K E F
601 TCCACCTGGTGGCTCTGGTGGCACCCAGGGACGGCATGCCGGGGGGCTGGCAAGGAGT

FIG. 1A



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115 S R S Y R L R Y S R D G R R W M G W K D
661 TCTCCGGAGCTACCGGCTTACTCCGGATGGCTGCCGCTGGATGGCTGAAGG

135 R W G Q E V I S G N E D P E G V V L K D
721 ACCGGCTGGGTCAGGAGGTGATCTCAGGCCAATGAGGAACCCCTGAGGGAGTGCTGAAGG

155 L G P P M V A R L V R F Y P R A D R V M
781 ACCTTGGCCCCCATGGTTGCCGACTGGCTCTACCCCCGGCTGACCGGGTCA

175 S V C L R V E L Y G C L W R D G L L S Y
841 TGAGTCGTCTGCTGGGTAGAGCTATGGCTGCCCTCTGGAGGGATGGACTCCTGCTT

195 T A P V G Q T M Y L S E A V Y L N D S T
901 ACACCGCCCTGTGGCAGACAATGTATTATCTGAGGCCGTACCTAACGACTCCA

215 Y D G H T V G G L Q Y G G L G Q L A D G
961 CCTATGACGGACATAACCGTGGGGACTGCAGTATGGGGTCTGGCCAGGTGGCAGATG

235 V V G L D D F R K S Q E L R V W P G Y D
1021 GTGTCGTGGCTGGATGACTTTAGGAAGAGTCAGGAGCTGGCTATGTGGAGATGGAGTTGAGT

255 Y V G W S N H S F S S G Y V E M E F E F
1081 ACTATGTCGTGGCTGGAGCAACCACAGCTTCCAGTGGCTATGTGGAGATGGAGTTGAGT

FIG. 1B



Axel ULLRICH et al.
DNA ENCODING MCK-10, A NOVEL
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275 D R L R A F Q A M Q V H C N N M H T L G
1141 TTGACCGGGCTGAGGGCCATTCCAGGCCATATGCCAGGTCCACTGTAACAAACATGCCACACGCTGG

295 A R L P G G V E C R F R R G P A M A W E
1201 GAGCCCCGTCTGGCCTGGGAATGTCGGCTTCCGGGCTGGCATGGCCTGGCTGG

315 G E P M R H N L G G N L G D P R A R A V
1261 AGGGGGAGGCCATGCCAACCTAGGGGCAACTGGGACCCCAGAGCCCCAG

335 S V P L G G R V A R F L Q C R F L F A G
1321 TCTCAGTGCCCCCTTGCGGGCGCTGGCTCGCTTCTGCAGTGCCGCTTCCTTGGCG

355 P W L L F S E I S F I S D V V N N S S P
1381 GGGCCCTGGTTACTCTTCAGGAAATCTCTTCATCTGTAATTCCTCTC

375 A L G G T F P P A P W W P P G P P T N
1441 CGGCACCTGGAGGCACCCCTTCCAGGCCAGGGCCCTGGTGGCCACCTCCACCA

395 F S S L E L E P R G Q Q P V A K A E G S
1501 ACTTCAGCAGGCTTGGAGCTGGAGCCAGGGCCAGGCCAGGAGGGCAAGGCCAGGGGA

415 P T A I L I G C L V A I I L L L L I I
1561 GCCCGACCGCCATCCTCATCGGCTGGCCATCATCCCTGCTGCTCATCA

FIG.1C



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435 A L M L W R L H W R R L L S K A E R R V
1621 TTGCCCTCATGCTCTGGGGCTGCAC TGCGGCAGGGCTCCTAGCAAGGCTGAACGGAGGG

455 L E E E L T V H L S V P G D T I L I N N
1681 TGTGGAAAGAGGAGCTGACGGTTCACTCTGGGGACACTATCCTCATCAACA

475 R P G P R E P P Y Q E P R P R G N P P
1741 ACCGCCAGGT CCTAGAGGGCCACCCCCGTACCCAGGAGCCATGGCTCGTGGAAATCCGC

495 H S A P C V P N G S A L L L S N P A Y R
1801 CCCACTCCGGCTCCCTGTGTCCTGCTGCTGCTCGTCCAAATCCAGGCTTACCC

515 L L L A T Y A R P P R G P G P P T P A W
1861 GCCTCCCTCTGCCACTTACGCCCTACGCCCTACAGTGCGGACTATACCCGCC

535 A K P T N T Q A Y S G D Y M E P E K P G
1921 GGGCAAACCAACAACCCAGGGCTACAGTGCGGACTATATGGAGGCCCTGAGAACCCAG

555 A P L L P P P Q N S V P H Y A E A D I
1981 GGGCCCGCTCTGGCCCCACCTCCAGAACAGGGCTCCATTATGCCAGGGCTGACA

575 V T L Q G V T G G N T Y A V P A L P P G
2041 TTGTTACCCCTGCAAGGGCTCACCGGGCAACACCCATTATGCTGTGCACTGCCAG

FIG. 1D



595 A V G D G P P R V D F P R S R L R F K E
2101 GGGCAGTCGGGATGGCCCCCAGAGTGGATTCCCTCGATCTGACTCGCTCAAGG

615 K L G E G Q F G E V H L C E V D S P Q D
2161 AGAAGCTTGGCAGGGCCAGTTGGGAGGTGCACCTGAGGTCACAGGCCCTCAAGG

635 L V S L D F P L N V R K G H P L L V A V
2221 ATCTGGTCAGTCTTGATTTCCCCCTTAATGTGCGTAAGGGACACCCTTGTAGCTGCT

655 K I L R P D A T K N A S F S L F S R N D
2281 TCAAGATCTTAGGGCCAGATGCCACCAAGAAATGCCAGCTTCCTTGTTCTCCAGGAATG

675 F L K E V K I M S R L K D P N I I R L L
2341 ATTTCCTGAAAGAGGTGAAGATCATGTCGAGGCTCAAGGACCCAACATCATTCGGTGC

695 G V C V Q D D P L C M I T D Y M E N G D
2401 TGGCGGTGTTGGACGGACCCCTCTGCATGATTACTGACTACATGGAGAACGGCG

715 L N Q F L S A H Q L E D K A A E G A P G
2461 ACCTCAACCAGTTCCCTCAGTGGCCCACAGCTGGAGGACAAGGCAGGGGGCCCTG

735 D G Q A A Q G P T I S Y P M L L H V A A
2521 GGGACGGGCAGGGCTGGCCAGGGCCACCATCAGCTACCCAAATGCTTGCTAGTGGCAG

FIG. 1E



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755 Q I A S G M R Y L A T L N F V H R D L A
2581 CCCAGATGCCCTCGGCATGGCTATCTGGCACACTCAACTTGTACATGGGACCTGG

775 T R N C L V G E N F T I K I A D F G M S
2641 CCACGGAAACTGCCCTAGTTGGGGAAATTTCACCATAAAATCCGAGACTTGGCATGA

795 R N L Y A G D Y R V Q G R A V L P I R
2701 GCCGGAACCTCTATGCTGGGGACTATTACCGTGTGCAGGGGGCAGTGCTGCCCATCC

815 W M A W E C I L M G K F T T A S D V W A
2761 GCTGGATGCCCTGGGAGTGCAATCCTCATGGGAAGTTCACGACTGGGAGGTGACGTGTGGG

835 F G V T L W E V L M L C R A Q P F G Q L
2821 CCTTGTGTGACCCCTGTGGAGGTGCTGATGCTCTGTAGGGCCCAGGCCCTTGCCAGGC

855 T D E Q V I E N A G E F F R D Q G R Q V
2881 TCACCGACGAGCAGGTCAATCCGAGAACGGGGAGATTCTCCGGACCGGGGGCAGG

875 Y L S R P P A C P Q G L Y E L M L R C W
2941 TGTACCTGTCCGGGGCCTGGCTGGCCAGGGCTATATGAGCTGATGCTTCGGTGCCT

895 S R E S E Q R P P F S Q L H R F L A E D
3001 GAGCCGGAGGTCTGAGGAGCCACCCCTTTCCAGCTGGCATGGCAGAGG

FIG. 1F



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915 A L N T V
3061 ATGCCACTAACACACGGTGTGAATCACACATCCAGGCTGCCCTCAGGGAGTGATCCAG

3121 GGGAAAGCCAGTGACACTAAACAAAGAGGACACAATGGCACCTCTGCCCTTCCCCTCCCCGA
3181 CAGCCCCATCACCTCTTAATAGAGGCAGTGAGACTGCAGGTGGCTGGGGCTGGGGCAACCCAGGGAG
3241 CTGATGCCCTCTCCCTCTGGACACACTCTCATGTCGCCCTGGATGGATGGATCCACCCCTCTCC
3301 TAGAAGGCCCTTGGGAAAGGGTGGAGAAATTAGGATAGACACTGGACATGGCCCATTTG
3361 AGCCATCCCTTGGGAAAGGGTGGAGAAATTAGGATAGACACTGGACATGGCCCATTTG
3421 GAGCACCTGGCCCCACTGGACAAACACTGATTCCTGGAGGGTGGCTGGGGCAAGGCTTC
3481 TCTCTCCCTGTACACACTGGACCCACTGGCTGAGAATTCTGGGGTGGAGGACAAGA
3541 AGGAGAGGAAATGTTCCCTGTGCCTGTACTTGTACTCTGGCTTGGCTTGGCTTC
3601 CTCCTCCATCACCTGAAACACTGGACCTGGGGTAGCCCCAGCCCCAGCCCTCAGTCACCC
3661 CCACTTCCCACCTTGAGCTTGAACCTCTAAGCCTATACGTTTCTGGAG
3721 TAAATATTGGGATTGGGGAAAGAGGGAGCAACGGGGCATAGCCCTGGGGTGGACATC
3781 TCTAGTGTAGCTGCCACATTGATTCTATAATCACTTGGGTTGTACATTGGGG
3841 GGAGAGACACAGATTACACTAATATGGACCTAGCTTGAGGCAATTAAATCCCT
3901 GCACTAGGCAGGTAATAAAAGGTGAGTTCCACAAAAAAACCGGAAT
3961 TC

FIG. 1 G



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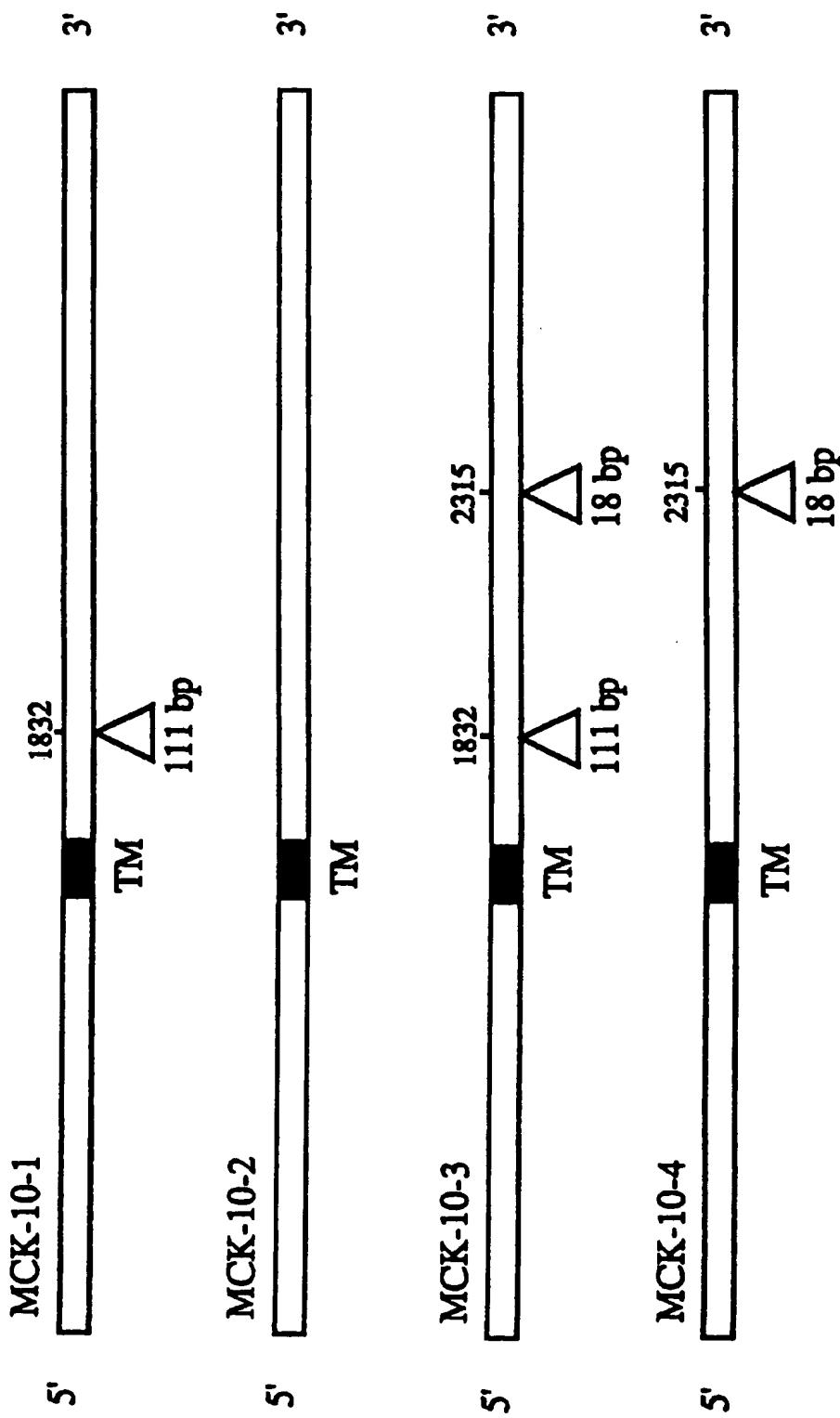
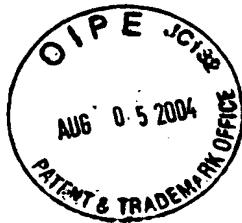


FIG.2



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FIG.3A



	542	gccccatatggaaaggctggactcagaagaaggggatggggccctggtgccctgagatcca	601
		cggtttatcaccttccgacctggatcttccttccctacclggaccacggacttcaagg	
b		A K Y G R L D S E E G D G A W C P E I P -	
	602	gtggaaacctgtatggacttggaggatllctgcagatgtacttgcacaccctccatllatc	661
		caccttggactatggacttccctaaatggacttgcacatggatggggaggtaaaatag	
b		V E P D D L K E F L Q I D L H T L H F I -	
	662	acttgggtggggaccctggggcgcccgatggatggatcgatggatggatggatggatgg	721
		tggatggaccacccctgggtccccggctcgatccatggatggatggatggatggatgg	
b		T L V G T Q G R R A G G H G I E F A P M -	
	722	tataatggatggatggatggatggatggatggatggatggatggatggatggatggatgg	781
		atggatggatggatggatggatggatggatggatggatggatggatggatggatggatgg	
b		Y K I N Y S R D G T R W I S W R N R H G -	
	762	aaacagggtggatggatggatggatggatggatggatggatggatggatggatggatgg	841
		tttgcacgcacccatggatggatggatggatggatggatggatggatggatggatgg	
b		K Q V L D G N S N P Y D I F L K D L E P -	
	842	cccatggatggatggatggatggatggatggatggatggatggatggatggatggatgg	901
		ggatggatggatggatggatggatggatggatggatggatggatggatggatggatgg	
b		P I V A R F V R F I P V T D H S M N V C -	
	902	atggatggatggatggatggatggatggatggatggatggatggatggatggatggatgg	961
		tatctcacctcgaaatggccGACACAGACCGATCTACCGAACCAACAGAAATGTTACGGT	
b		M R V E L Y G C V W L D G L V S Y N A P -	

FIG.3B



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RECEPTOR TYROSINE
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962	GCTGGGCACCAAGTTGACTCCCTGGAGGTCCATCATTATCTGAATGATTCTGTCTAT CGACCCGTCGTAAACATGAGGGACCTCAAGGTAGTAAATAGACTTACTAAGACAGATA	1021
b	A G Q Q F V L P G G S I I Y L N D S V Y -	
1022	GATGGAGCTGTTGGATACAGCATGACAGAAGGGCTAGGCCATTGACCGATGGTGTCT CTACCTCGACAACCTATGTCGTACTGTCTTCCCCTAACGGCTACCGTACACACAGA	1081
b	D G A V G Y S M T E G L G Q L T D G V S -	
1082	GGCCTGGACCATTCACCCAGACCCATGAATACCACGTGTGGCCGGCTATGACTATGTG CCGGACCTGCTAAAGTGGGTCTGGGTACTTATGGTGACACCGGGCCGATACTGATAACAC	1141
b	G L D D F T Q T H E Y H V W P G Y D Y V -	
1142	GGCTGGCCAACGAGACTGCCACCAATGGCTACATTGAGATCATGTTGAATTGACCGC CCGACCCGCTTGCTCTACGGTGCTTACCGATGTAACTCTAGTACAAACTAAACTGGCG	1201
b	G W R N E S A T N G Y I E I M F E F D R -	
1202	ATCAGGAATTCACTACCATGAAGGTCCACTGCAACAAACATGTTGCTAAAGGTGTGAAG TAGTCCTTAAACTGCGTACTTCCAGGTGACGTTGTTGACAAACGATTCCACACTTC	1261
b	I R N F T T M K V H C N N M F A K G V K -	
1262	ATCTTTAAGGAGGTACAGTGCTACTTCCGCTCTGAAGCCAGTGACTGGTACCTAATGCC TAGAAATTCCCTCATGTCACGATGAAGGCGAGACTTCCGTCACTCACCCATGGATTACGG	1321
b	I F K E V Q C Y F R S E A S E W V P N A -	
1322	ATTTCCCTcccccttgtcctggatgacgtcaaccccgagtgcgtcggttgtcgcgggtgcct TAAAGGAAgggggoacaggccactgcagllgggtcacgagccaaacogtgccacggaa	1381
b	I S F P L V L D D V N P S A R F V T V P -	

FIG.3C



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1382	c t c c a c c a c c g a a l g g c c a g l g c c a t c a a g t g t c a a t c c a c t t t g c a g a l a c c t g g a t g g a g g l g g g c t t a c c g g t c a c g g l g a g t t c a c a g t t a t g g t a a a o c g t c t a t g g a c c l a c L H H R M A S A I K C Q Y H F A D T W M -	1441
1442	a t g t t c a g t g a g a t c a c c t t c c a a l c a g a t g c a a t g t a c a a c a c t t c t g a a g c c t g t a c a a g t t c a c t t c a g t g g a a g g t t a g t t c a c g a c t t a c a t g t t g a g a c t t c g g g a c M F S E I T F Q S D A A A M Y N N S E A L -	1501
1502	c c c a c c t t c c t a l g g c a c c c a a c c t a t g a t c c a a l g c t t a a a g t t g a l g a c a g c a a c g g g l g g g a g g a l a c c g l g g g t t g g a t a c l a g g t t a c g a a l l t c a a c t a c t g t c g t g P T S P M A P T T Y D P M L K V D D S N -	1561
1562	a c t c g g a t c c t a l g g c l g c t t g g c c a l c a t t t a t c c t c l g g c c a l c a t t g c t g a g c c t a g g a c t a a c c g a c g a a c c a c c g g t a g t a g a a a t a g g a g g a c c g g t a g t a a c g T R I L I G C L V A I I F I L L A I I V -	1621
1622	a t c o t c c t t l g g a g g c a g t t c g g c a g a a a a l g t g g a g a a g g c t t c g g a g g a t g c t g t a g t a g g a g a c c t c c g t c a a g a c c g t t t t a c g a c c t t c c g a a g a g c c t c c t a c g a c I I L W R Q F W Q K M L E K A S R R M L -	1681
1682	g a t g a a a t g a c a g l c a g c c t t t c c t l g c c a a g t g a t t c c a g c a l g t t c a a c o o t a a c c t a c t a c t t a c t g t c a g t c g g a a a g g g a c g g t t c a c t a a g a t c g t a c a a g t t g t t t t g D D E M T V S L S L P S D S S S M F N N N -	1741
1742	c g t t c c t c a t c a c c t o g l g a a c a a g g g t c c a a c t c g a c t t a c g a t c g c a t t t t c c c t t g c g a g g g a g g a g g a t c a c t t t c c c a g g t t g a g c t g a a t g c l o g c g t a g a a a g g g g a a R S S S P S E Q G S N S T Y D R I F P L -	1801

FIG.3D



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	cgccctgactacCAGGAGCCATCCAGGCTGATACGAAAACCTCCAGAATTGCTCCAGGG	1861
1802	gcgggactgatgGTCTCGGTAGGTCCGACTATGCTTTGAGGTCTTAAACGACGTCCC	
b	R P D Y Q E P S R L I R K L P E F A P G	-
	GAGGAGGAGTCAGGCTCCAGCGGTGTTGTAAGCCAGTCCAGCCCAGTGGCCCTGAGGG	1921
1862	CTCCTCCTCAGTCCGACCTCGCCACAACACTTCGGTCAGGTGGTCAACGGGACTCCCC	
b	E E E S G C S G V V K P V Q P S G P E G	-
	GTGCCCCACTATGCAGAGGCTGACATACTGAACCTCCAAGGAGTGACAGGAGGAAACACA	1981
1922	CACGGGGTGTACGTCCGACTGTATCACTTGGACCTCCCTCACTGTCCCTCGTTGT	
b	V P H Y A E A D I V K L Q G V T G G N T	-
	TACTCAGTGCCTGCCCTCACCATGGACCTGCTCTCAGGAAAACATGTGGCTGTGGAGGAG	2041
1982	ATGACTCACGGACGGCAGTGGTACCTGGACGAGTCCTTTCTACACCGACACCTCCTC	
b	Y S V P A V T M D L L S G K D V A V E E	-
	TTCCCCAGGAAACTCTAACTTCAAAGACAAGCTGGGACAAGGACAGTTGGGAGGTT	2101
2042	AAGGGTCTTTGAGGATTGAAAGTTCTCTCGACCCCTTCCGTCAAACCCCTCCAA	
b	F P R K L L T F K E K L G E G Q F G E V	-
	CATCTCTGTGAAGTGGAGGAAATGAAAAATTCAAAGACAAGATTTGCCCTAGATGTC	2161
2102	GTACAGACACTTCACCTCCCTAACCTTTAAGTTCTGTTCTAAACGGGATCTACAG	
b	H L C E V E G M E K F K D K D F A L D V	-
	ACTGCCAACCAACCAGCCTGCTGGCTGTGAAAATGCTCCGAGCAGATGCCAACAGAAT	2221
2162	TCACGGTTGGTGGACAGGACCCACCGACACTTCTACCGAGGCTCGTCTACGGTTGTTCTTA	
b	S A N Q P V L V A V K M L R A D A N K N	-

FIG.3E

2222 GCCAGGAATGATTTCTTAAGGAGATAAACATCATGTCTGGCTAAGGACCCAAACATC 2281
 CGGTCCCTACTAAAAGAATTCTCTATTCTAGTACAGAGCCGAGTCCTGGTTGTAG

b A R N D F L K E I K I M S R L K D P N I -

2282 ATCCATCTATTAGCTGCTGTATCACTGATGACCCCTCTCTGTATGATCACTGAATAACATC 2341
 TAGGTAGATAATCGACACACATAGTCACTGGAGAGACATACTACTGACTTATGTAC

b I H L L A V C I T D D P L C M I T E Y M -

2342 GAGAATGGAGATCTCAATCAGTTCTTCCCCCACGAGCCCCCTAATTCTCCTCCAGC 2401
 CTCTTACCTCTAGACTTAGTCAAAGAAAGGGCGTGCTCGGGGATTAAGAAGGAGGTCG

E N G D L N Q F L S R H E P P N S S S S -

2402 GATGTACCGACTGTCAGTTACACCAATCTGAAGTTATGGCTACCCAAATTGCCTCTGGC 2461
 CTACATGGTGACAGTCATGTGTTAGACTCAAATACCGATGGTTAACGGAGACCG

b D V R T V S Y T N L K F M A T Q I A S G -

2462 ATGAAGTACCTTCCCTCTTAATTTGTTACCGAGATCTGCCACACGAAACTGTTA 2521
 TACTTCATGCAAACGAGAGAATTAAACAAGTGGCTCTAGACCGGTGCTTGTACAAT

b M K Y L S S L N F V H R D L A T R N C L -

2522 GTGGGTAAAGAACTACACAATCAAGATAGCTGACTTTGGAATGAGCAGGAACCTGTACAGT 2581
 CACCCATTCTTGATGTGTTAGTTCTATCGACTGAAACCTTACTCGTCTTGGACATGTCA

b V G K N Y T I K I A D F G M S R N L Y S -

2582 GCTGACTATTACCGATCCAGGGGGGGGAGTGCTCCCTATCGCTGGATGTCCTGGAC 2641
 CCACTGATAATGGCCTAGGTCCCCGGCGTCACGAGGGATAGGGGACCTACAGAACCTC

b G D Y Y R I Q G R A V L P I R W M S W E -

FIG.3F



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	AGTATCTGCTGGCAAGTTCACTACAGCAAGTGATGTGGCCCTTGGGTTACTTG		
2642	<u> +</u> <u> +</u> <u> +</u> <u> +</u> <u> +</u>		2701
	TCA TAGA AC GAC CC GT TCA AGT GA TG C GT TCA CT AC AC ACC CG AA ACC CC AA TG AA AC		
b	S I L L G K F T T A S D V W A F G V T L -		
	T G G G A G A C T T C A C C T T T G T C A A G A A C A G C C T A T T C C A G C T G T C A C A T G A A C A G G T T		
2702	<u> +</u> <u> +</u> <u> +</u> <u> +</u> <u> +</u>		2761
	A C C C T C T G A A A C T G G A A A A C A G T C T T G T C G G G A T A A G G G T C C A G A C A G T C T A C T T G T C C A A		
b	W E T F T F C Q E Q P Y S Q L S D E Q V -		
	A T T G A G A A T A C T G G A G A G T T C T C C G A G A C C A A G G G A G G C A G A C T T A C C T C C T C A A C C A		
2762	<u> +</u> <u> +</u> <u> +</u> <u> +</u> <u> +</u>		2821
	T A A C T C T T A T G A C C T C T C A A G A A G G C T C T G G T T C C C T C C G T C T G A A T G G A G G G A G T T G G T		
b	I E K T G E F F R D Q G R Q T Y L P Q P -		
	G C C A T T T G C C T G A C T C T G T G T A A G C T G A T G C T C A G C T G C T G G A C A A G A G A T A C G A A G		
2822	<u> +</u> <u> +</u> <u> +</u> <u> +</u> <u> +</u>		2881
	C G G T A A A C A G G A C T G A G A C A C A T A T T C G A C T A C G G A G T C G A C G A C T C T T C T A T G C T T C		
b	A I C P D S V Y K L M L S C W R R D T K -		
	A A C C G T C C T C A T T C C A A G A A A T C C A C C T T C G C T C C T C A A C A A G G G C A C C G A G T G A T G C		
2882	<u> +</u> <u> +</u> <u> +</u> <u> +</u> <u> +</u>		2941
	T T G G C A G G G A G T A A G G T T C T T A G G T G C A A G A C G G A G A G T T G T T C C G T G C T C A C T A C C		
b	N R P S F Q E I H L L L L Q Q G D E -		
	T G T C A G T G C C T G G C C A T G T T C C T A C G G C T C A G G T C C T C C C T A C A A G A C C T A C C A C T C A C C		
2942	<u> +</u> <u> +</u> <u> +</u> <u> +</u> <u> +</u>		3001
	A C A G T C A C C G A C C G G T A C A A C G A T G C C G A G T C C A G G A G G G A T G T T C T G G A T G G T G A C T G G		
b	C A T G C C T A T G C C A C T C C A T C T G G A C A T T A A T G A A A C T G A G A G A C A G A C G C T T G T T G C T		
3002	<u> +</u> <u> +</u> <u> +</u> <u> +</u> <u> +</u>		3061
	G T A C C G A T A C C G T G A G C T A G A C C T G T A A A T T A C T T G A C T C T G T C T C C G A A C A A A C G A		

FIG. 3G



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b

3062 TTGCCCTCTTTCCCTGGTACCCCCACTCCCTACCCCTGACTCATATATACTTTTTTT
 +-----+-----+-----+-----+-----+-----+
 AACGGGAGAAAGGACCACTGGGGTGAGGGATGGGACTGACTATATGAAAAAAA
 3121

b

3122 TTACATTAAAGAACTAAAAAAAAAAAAAGGGC
 +-----+-----+-----+
 AATGTAATTCTTGATTTTTTTTTCCC
 3158

b

FIG.3H



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1	MILIPRMLLVLFLLPILSSA...KAQVNPAICRYPLGMSGCCQIPD EDIT ..MGPEALSSLLLLLVLASGDADMKHFDPAKCRYALGMQDRTIPDS DIS	47 CCK-2 48 MCK-10
48	ASSQWSESTA AKYGR LDSEEGDGAWCPEIPVVEPDOLKEFLQIDLHTLHF I : : .: : .: . . .: : : : 49 ASSSWSDSTAARHSRLESSDGDGAWCPAGSVFPKE.EEYLQVDLQLRLHLV	97 97
98	TLVGTQGRRAGGHGIEFAPMYKINYSRDGTRWI SWRNRHKGQVLDGNSNP . : .. .: : : .: .: : 98 ALVGTQGRHAGGLKEFSRSYRLRYSRDGRWWGKDRNGQEVI SGNEDP	147 147
148	YDIFLKDLLEPPIVARFVRFIPVTDHSMNVCMRVELYCCWLDGLVSYNAP ::: : : . . : . : : : . : 148 EGVVLKDLGPPMVARLVRFYPRADRVMSVCLRVELYGCWLW RDGLLSYTAP	197 197
198	AGQQFVLPGCSIIYLNDSVYDG.AVGYSMTEGLGQLTDGVSGLDDFTQTH . : .: : . . : . ..: 198 VGQTMYLSEA..VYLNNDSTYDGH TVGGLQYGGLGQLADGWGLDDFRKSQ	246 245
247	EYHWP GYDYVGWRNESATNGYIEIMFEFDRIRNFTTMKVHCNNMFAKGV .: . . : : : 246 ELRWP GYDYVGWSNHSFSSGYVEMEFDRIRAFQAMQVHCNNMHTLGA	296 295
297	KIFKEVQC.YFRSEASEWPN AISFPLVLDVNPSARFVTVPLHHRMASA ::: : . .: . .: . . . : 296 RLPGGVECRFRRGPMANAE GEPMRHNLGGNLGDPRARAVS VPLGGRVARF	345 345
346	IKCQYHFADTMMFSEITFQSDAAMYNNSEALPTS..... .: .: .: . .: . . . : 346 LQCRLFAGPWLLFSEISD.VWNNSSPALGGTFPPAPWWPPGPPP TN	380 394
381PMAPTTYDPMLKVDDSNTRILIGCLVAII FILLAIIVIILWROFWQ .: . .: .: . .: . .: . . : 395 FSSLELEPRGQQPVAKAEGSPTAILIGCLVAII LLLLII ALMLWRLHMR	426 TRANSMEMBRANE 444 REGION
427	KMLEKASRRMLDDEM T VSLSLPSDSSMFNNNRSSSPSEQGSNSTYDRIFP ::: .: .: . .: .: .: .: : 445 RLLSKAERRVLEEEELTVHL SVPGDTILINNRPGPREP.....	476 481

FIG.4A



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FIG.4B



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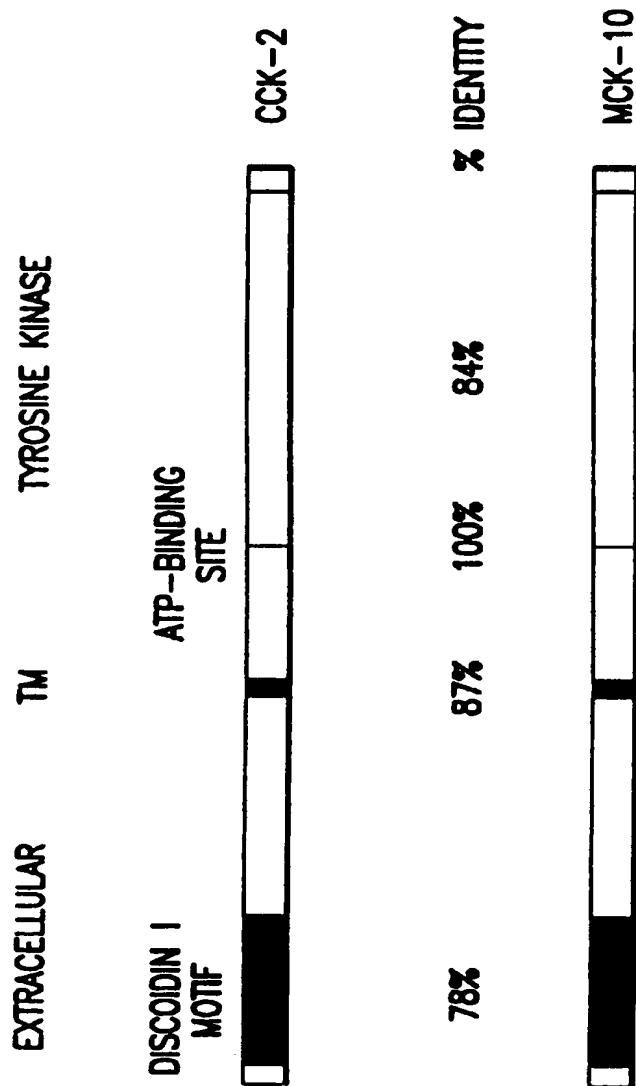
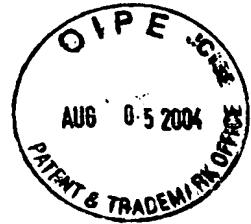


FIG. 4C



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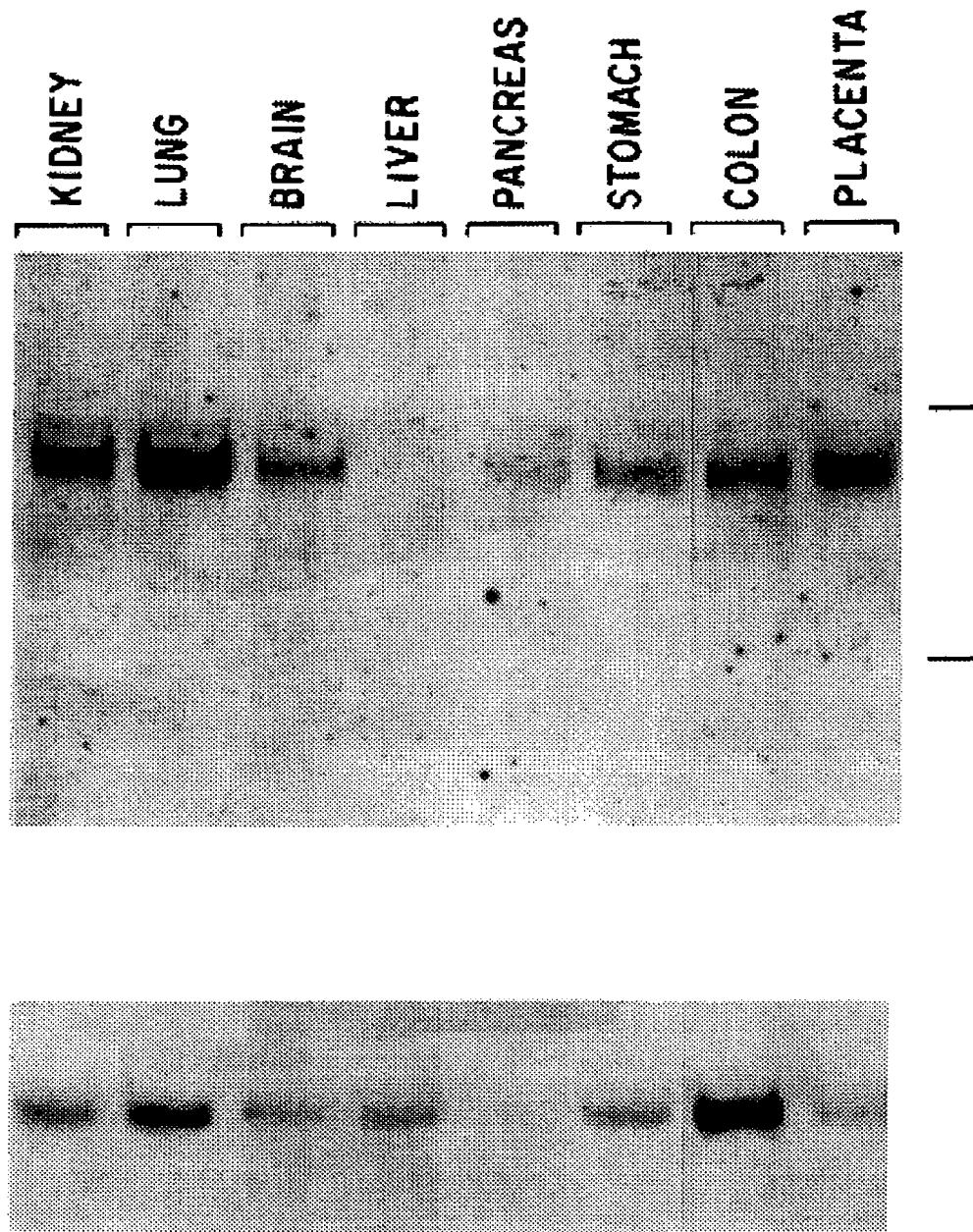


FIG.5A

AUG 10 2004



BT - 474
T - 47D
BT - 20
MDA - MB - 453
MDA - MB - 468
MDA - MB - 435
MDA - MB - 175
MDA - MB - 231
HBL - 100
SK - BR - 3
MCF - 7

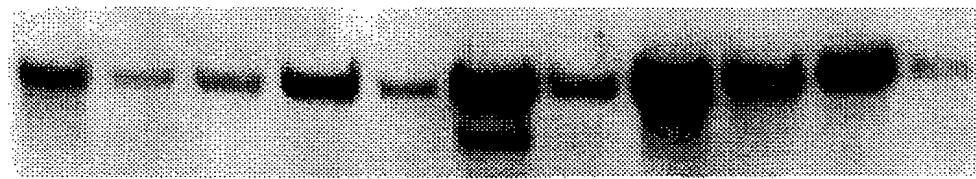
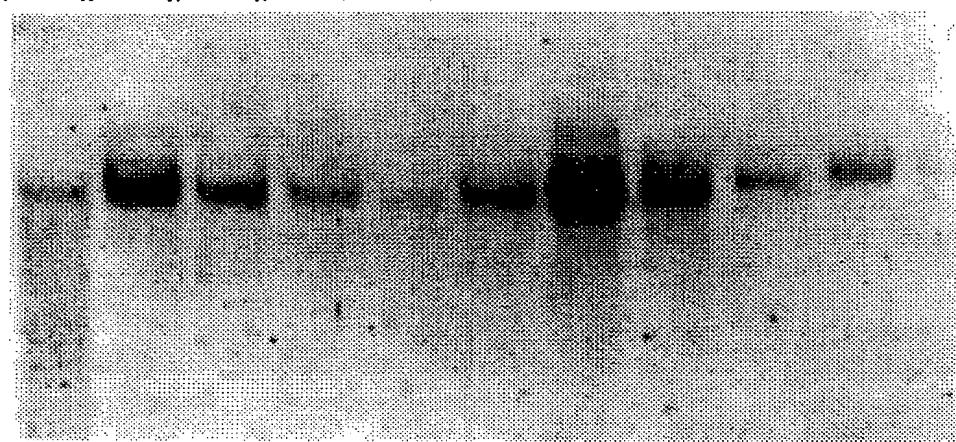


FIG. 5B



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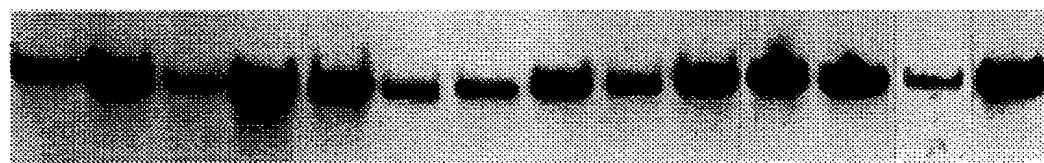
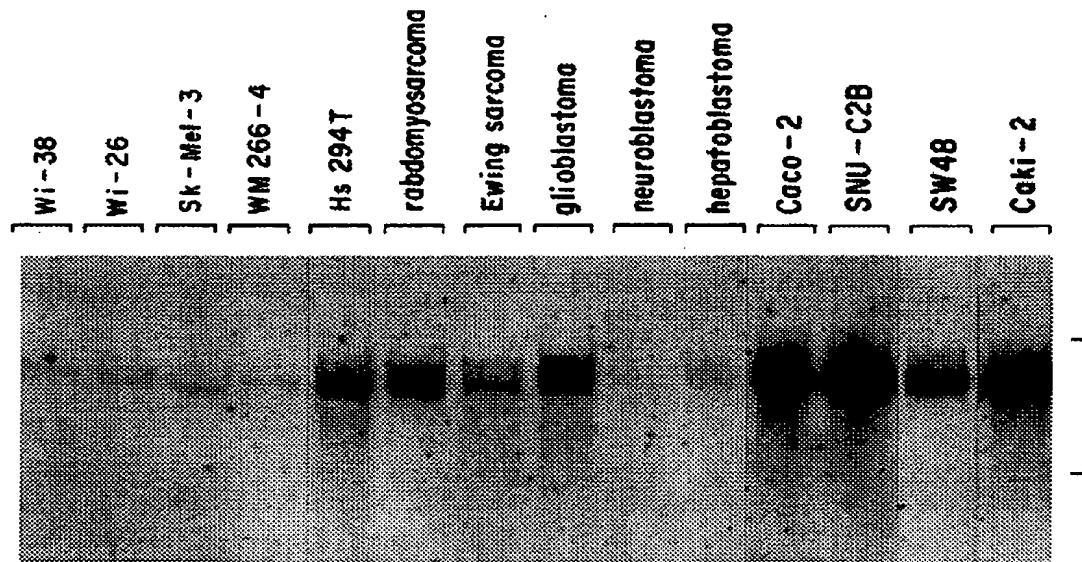


FIG.5C

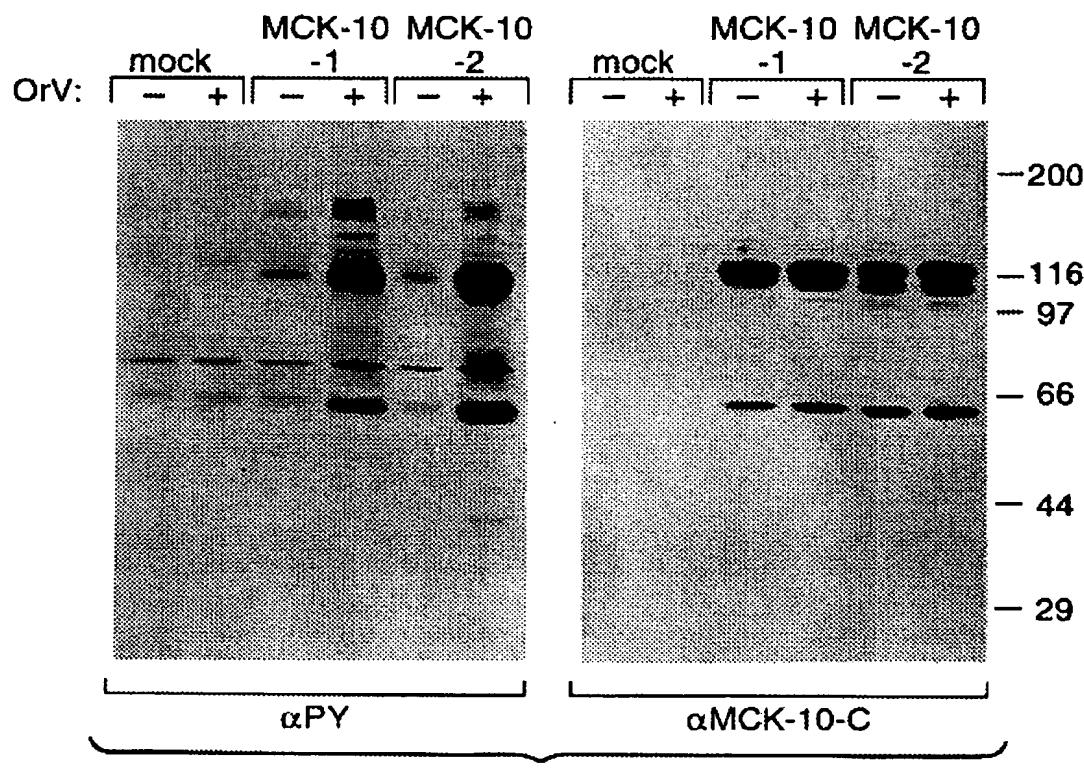


FIG.6A



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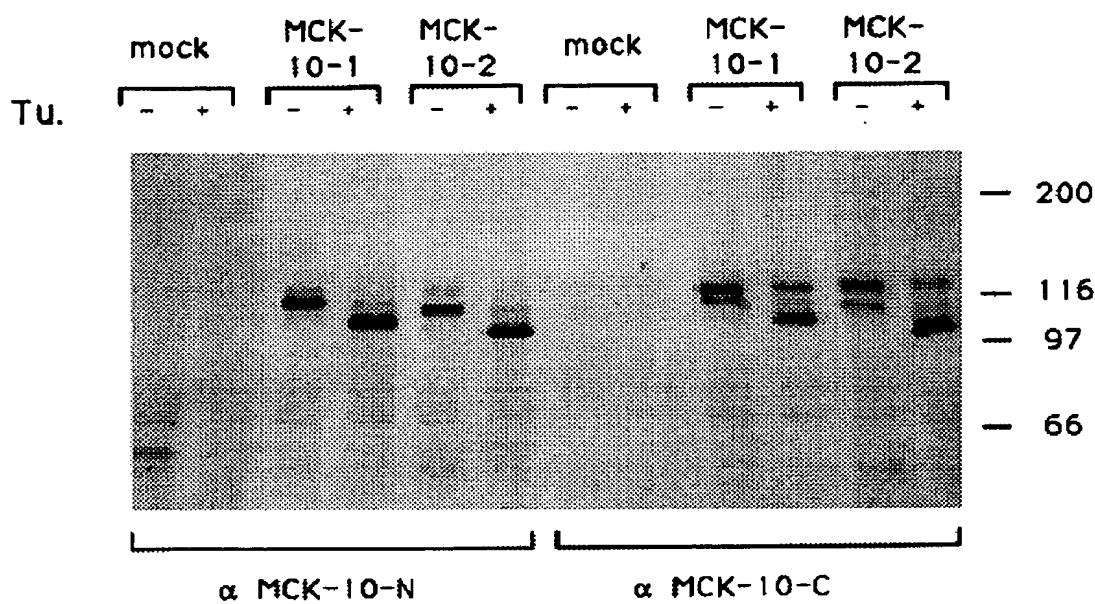
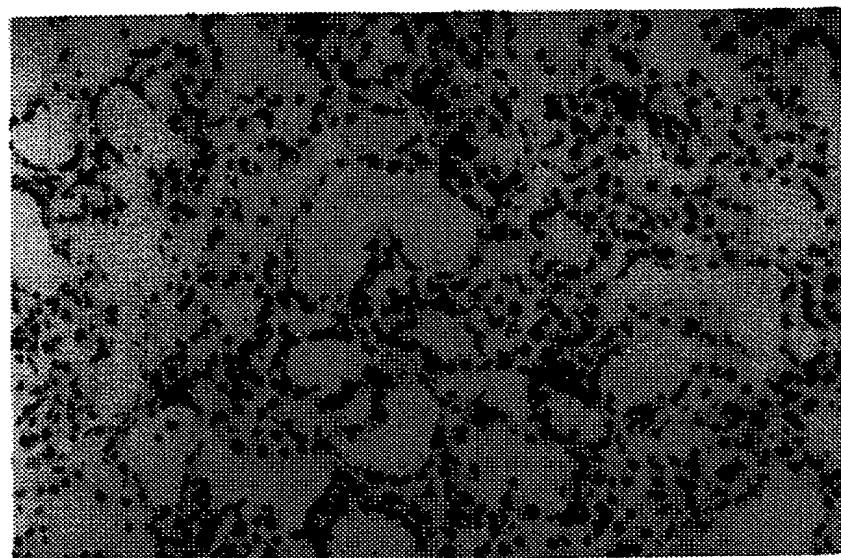
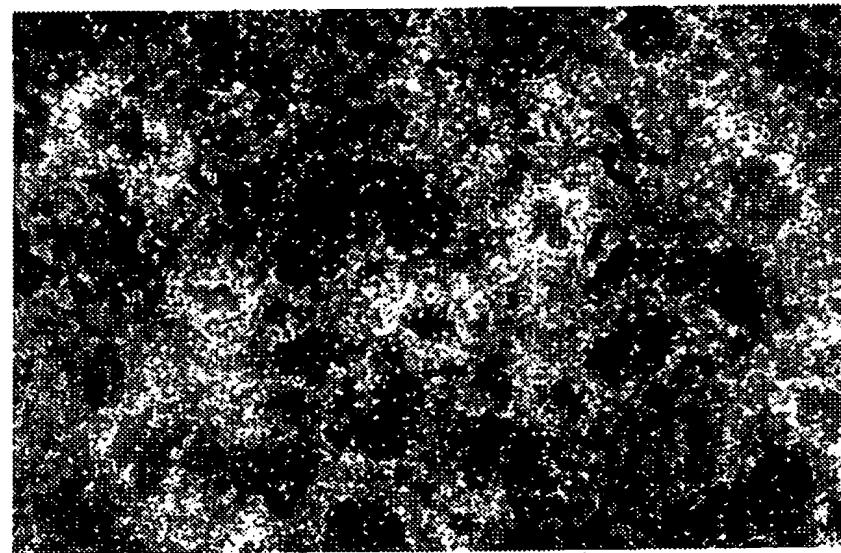


FIG.6B



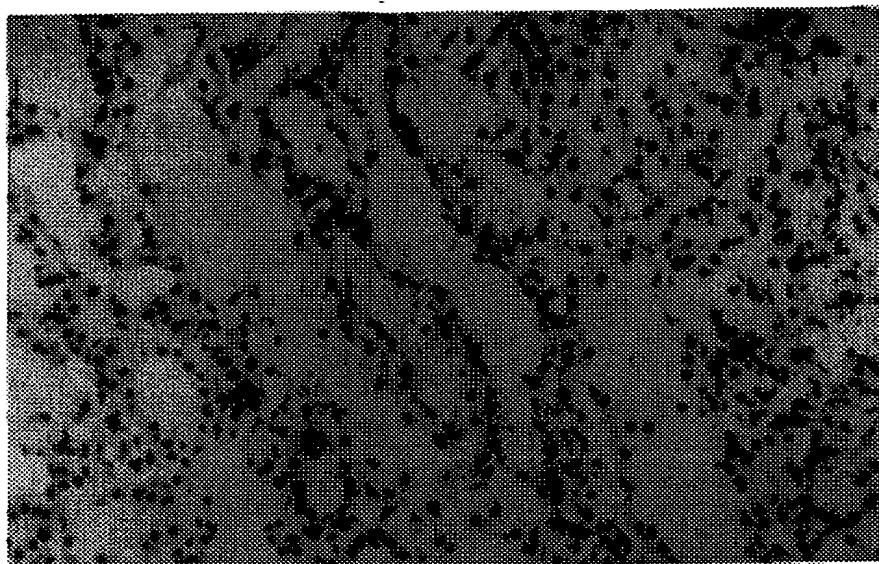
Lightfield

FIG. 7A



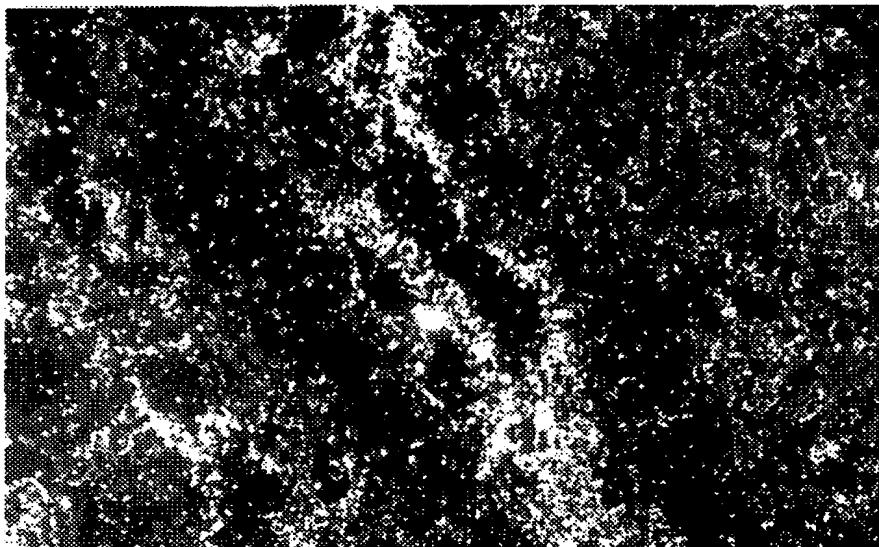
Darkfield

FIG. 7B



Lightfield

FIG.8A

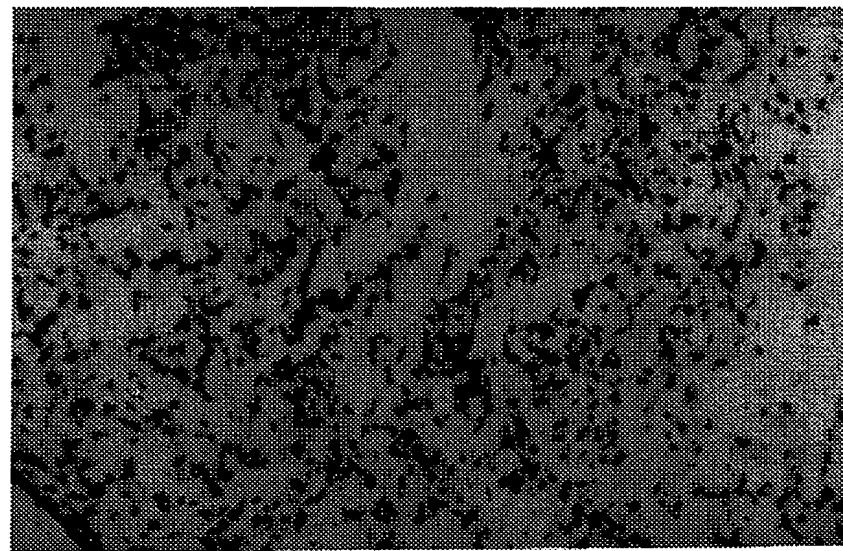


Darkfield

FIG.8B

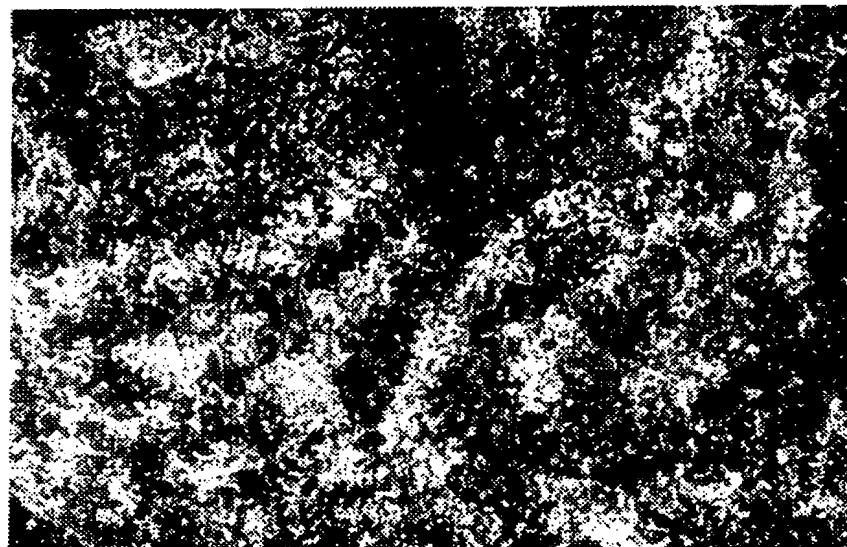


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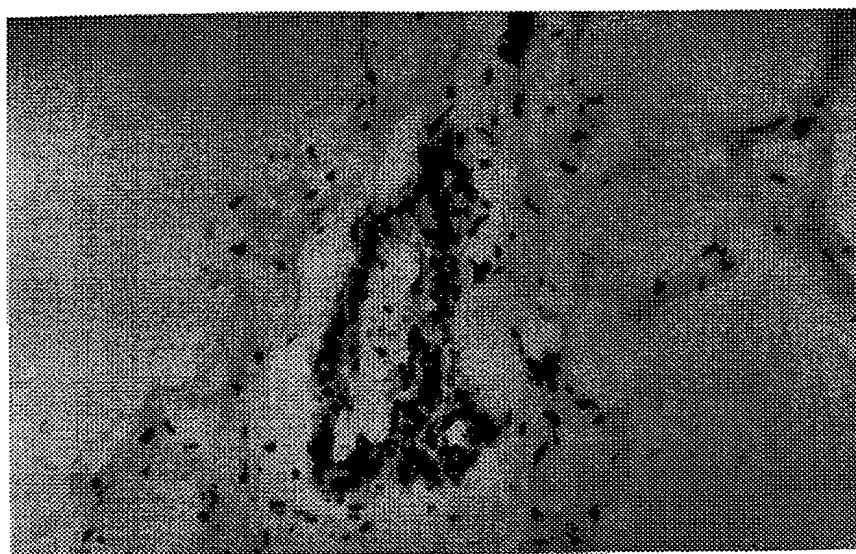
Lightfield

FIG.9A



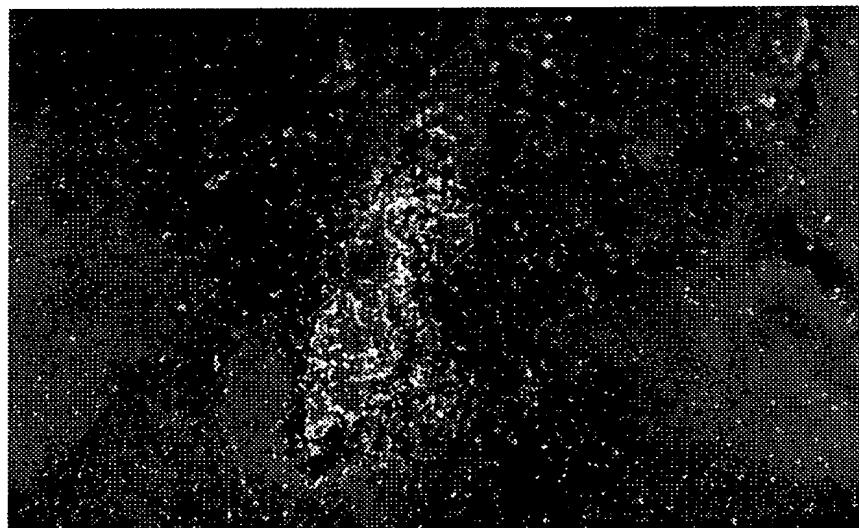
Darkfield

FIG.9B



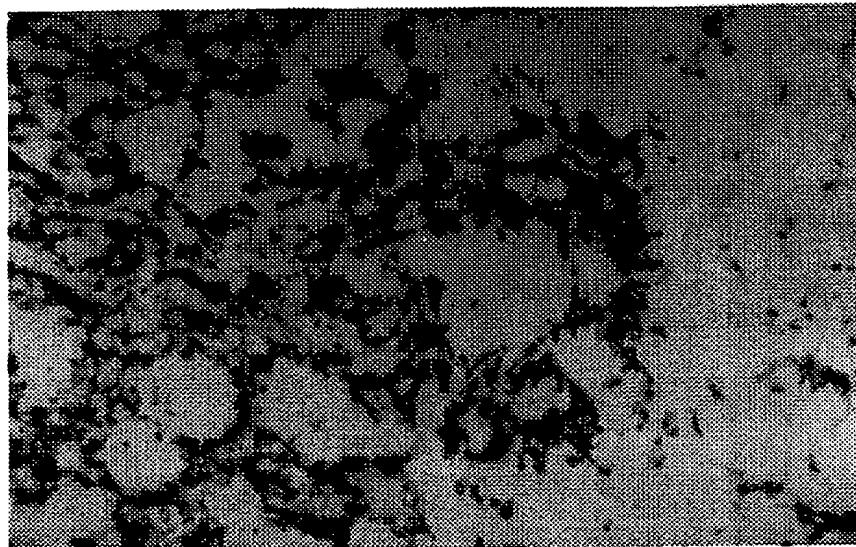
Lightfield

FIG.10A



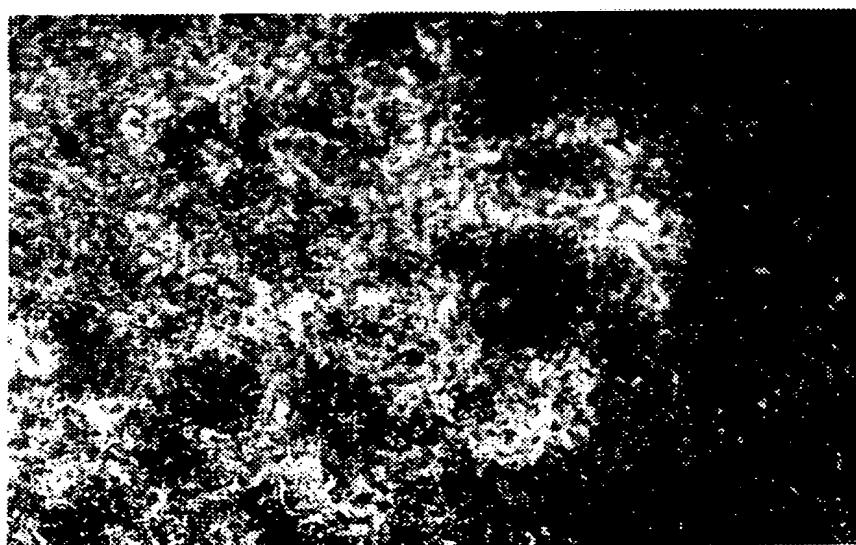
Darkfield

FIG.10B



Lightfield

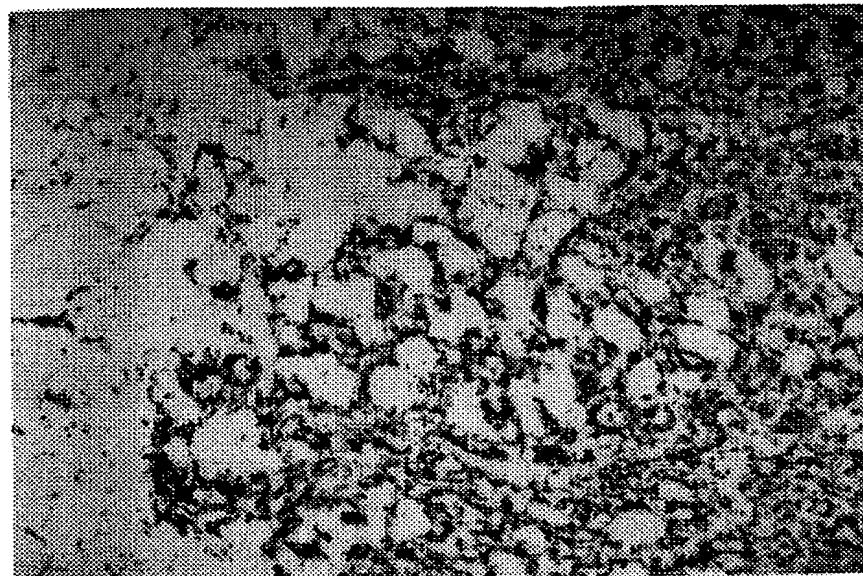
FIG.11A



Darkfield

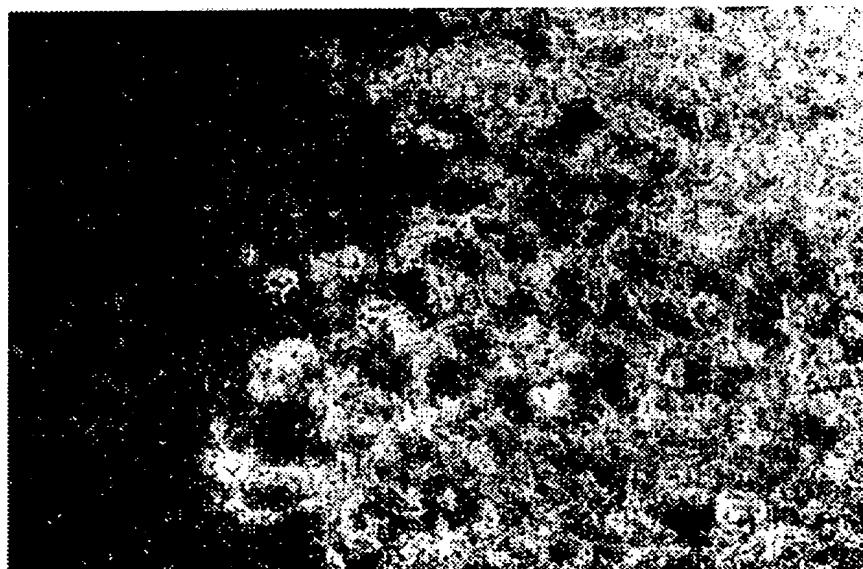
FIG.11B

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Lightfield

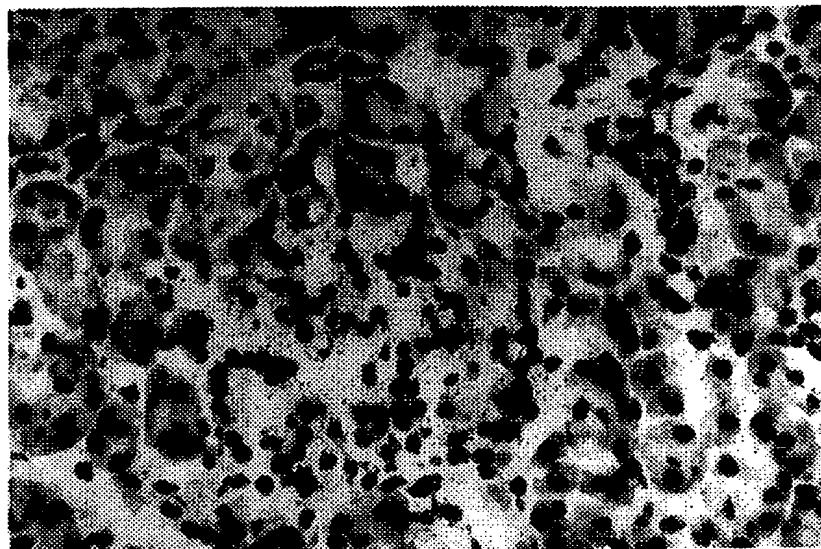
FIG.12A



Darkfield

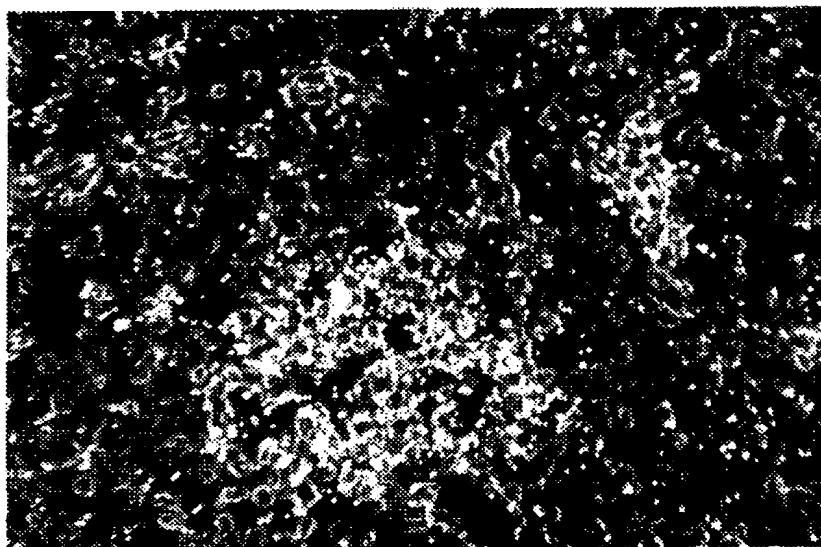
FIG.12B

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Lightfield

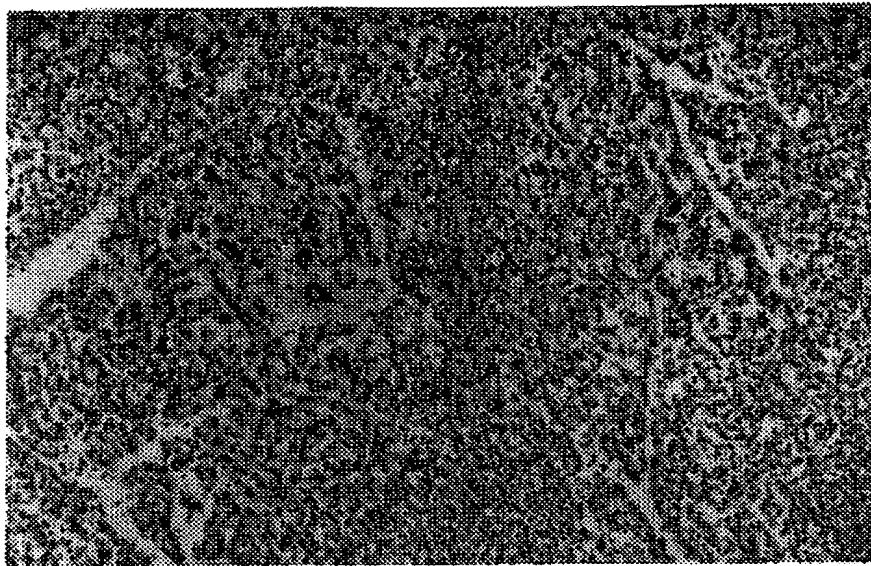
FIG.13A



Darkfield

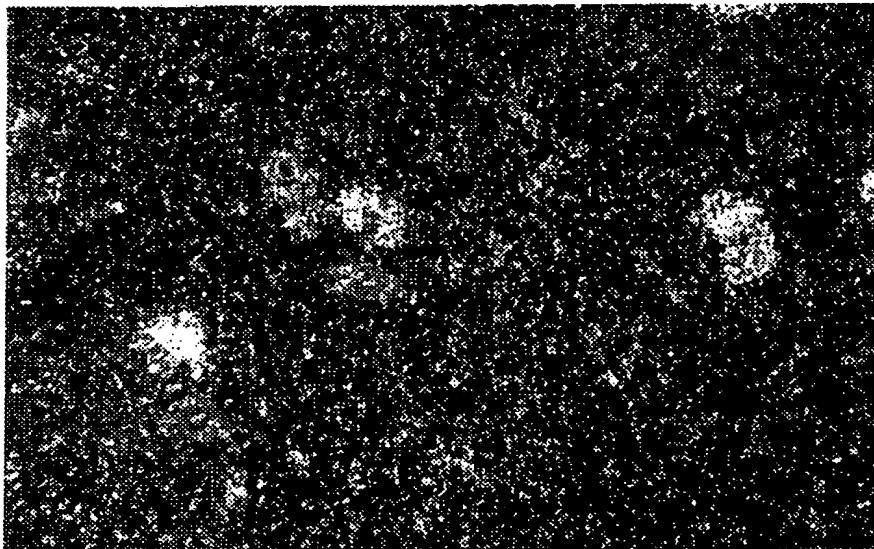
FIG.13B

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Lightfield

FIG. 14A



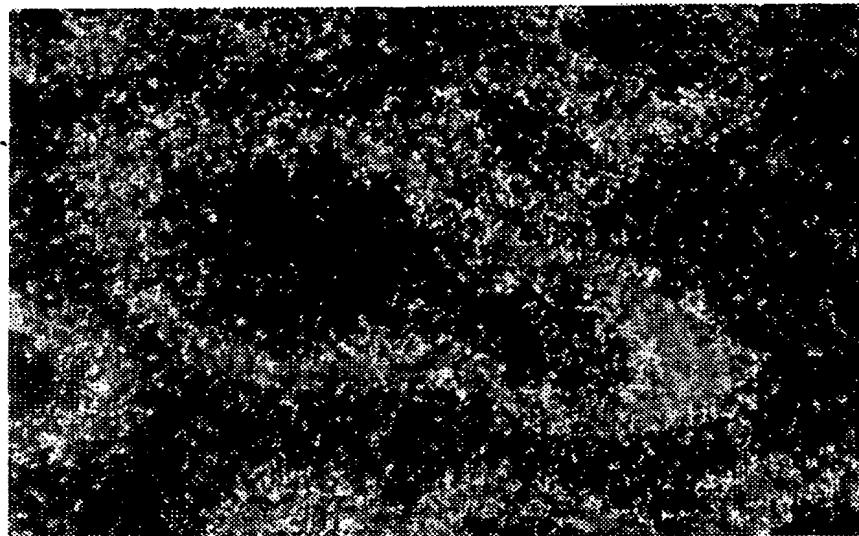
Darkfield

FIG. 14B



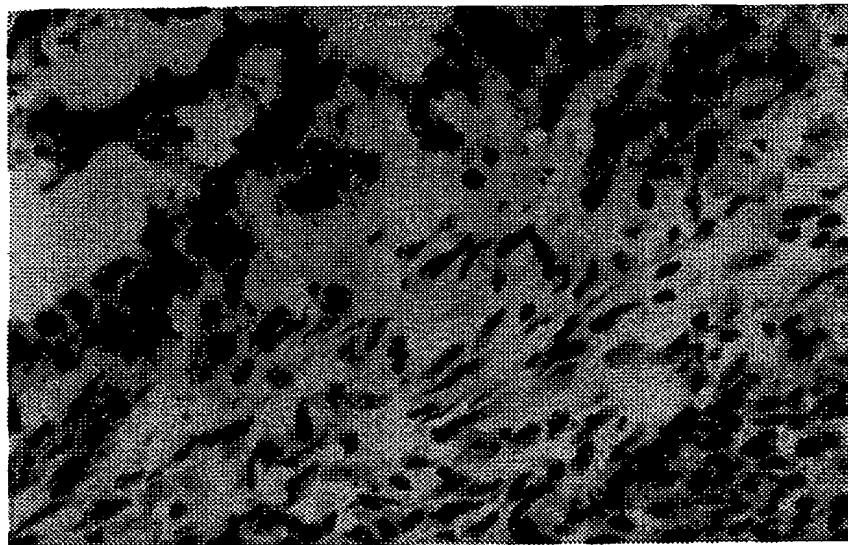
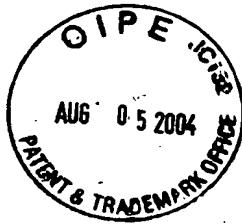
Lightfield

FIG. 15A



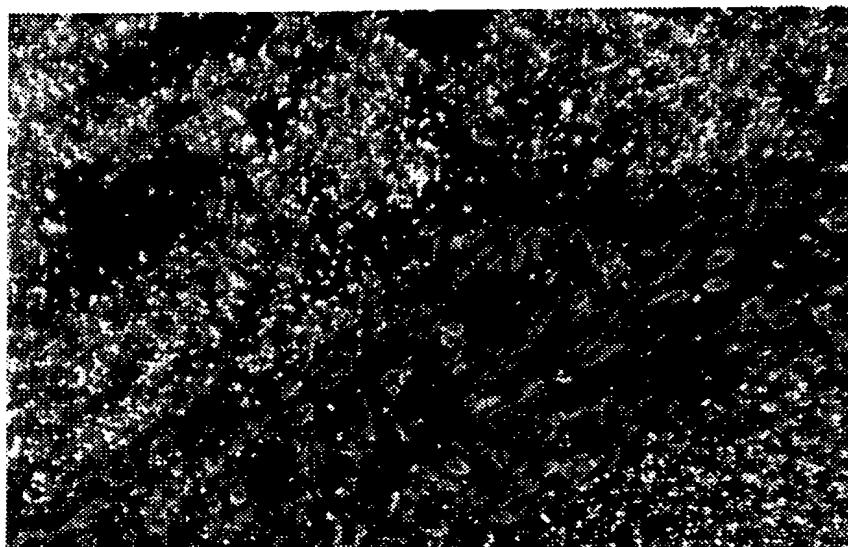
Darkfield

FIG. 15B



Lightfield

FIG.16A



Darkfield

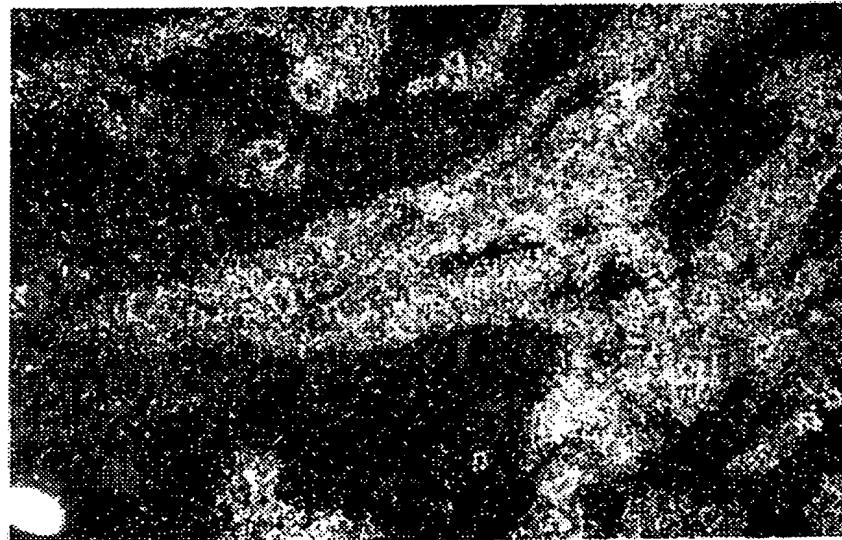
FIG.16B

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Lightfield

FIG.17A



Darkfield

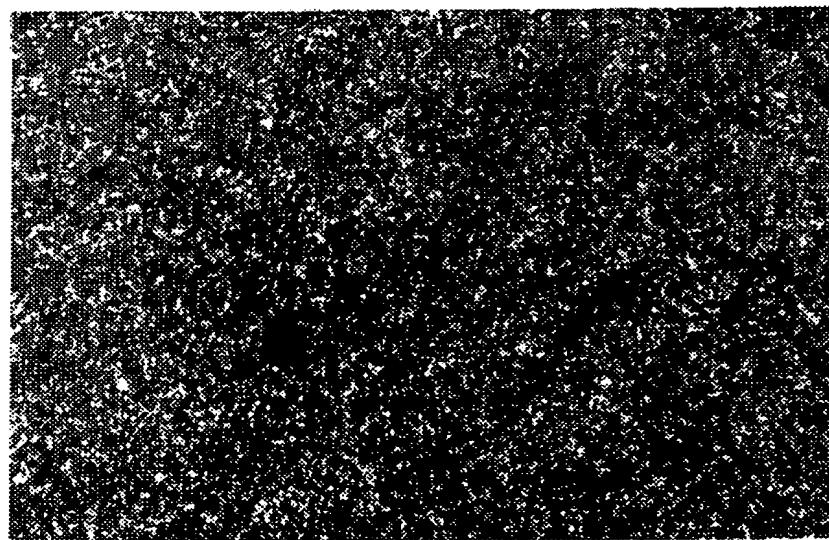
FIG.17B

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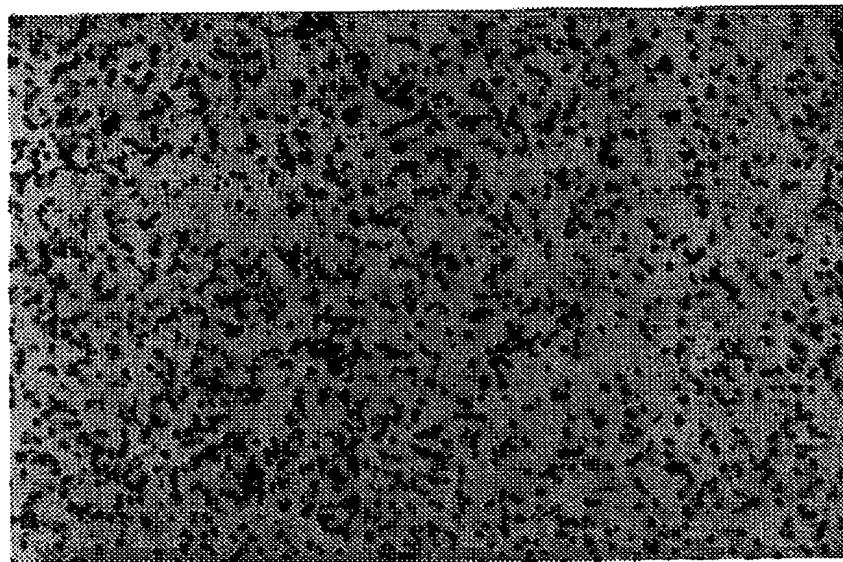
Lightfield

FIG.18A



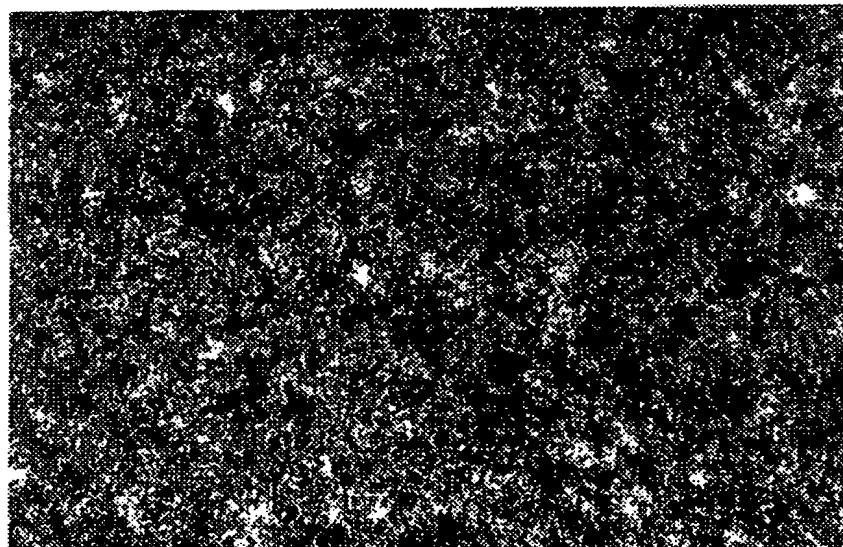
Darkfield

FIG.18B



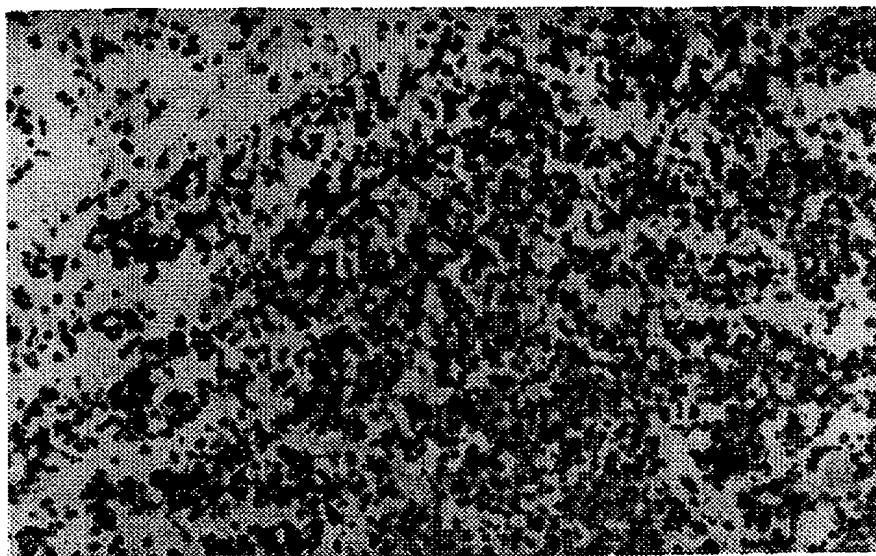
Lightfield

FIG.19A



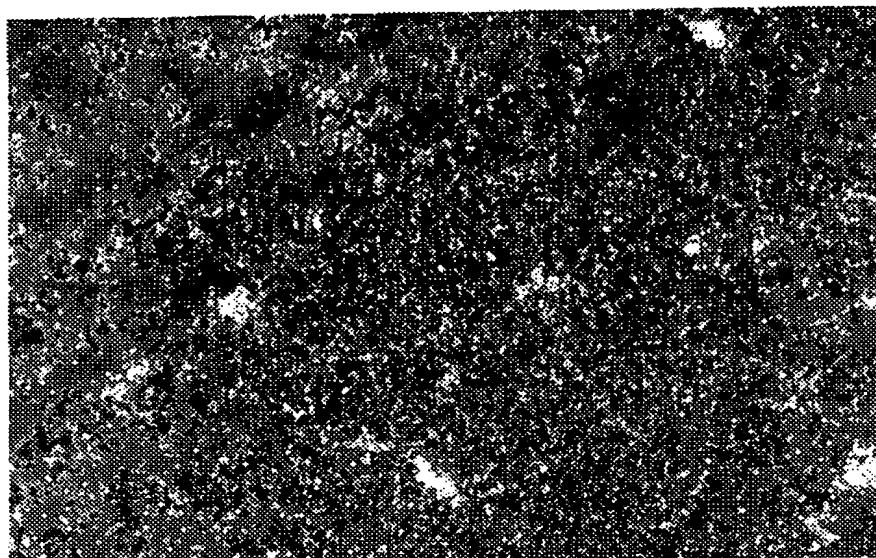
Darkfield

FIG.19B



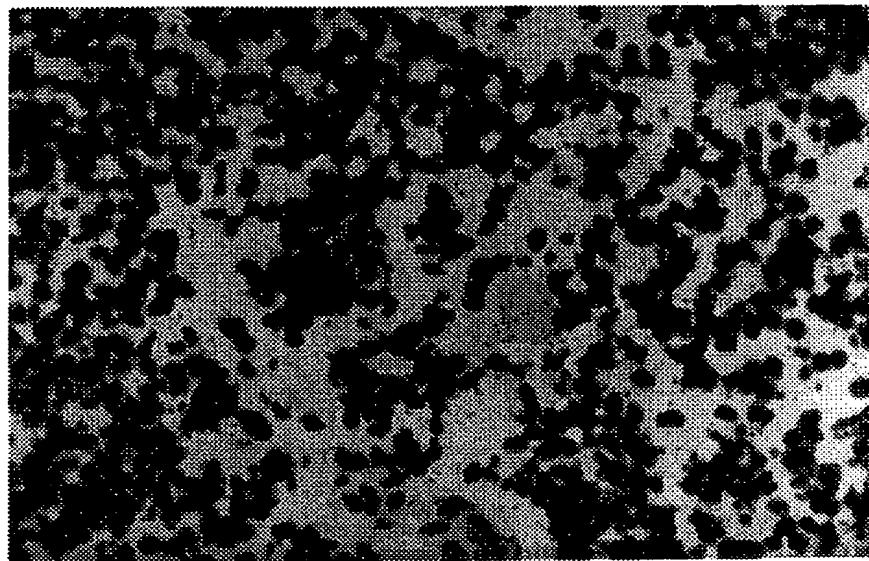
Lightfield

FIG. 20A



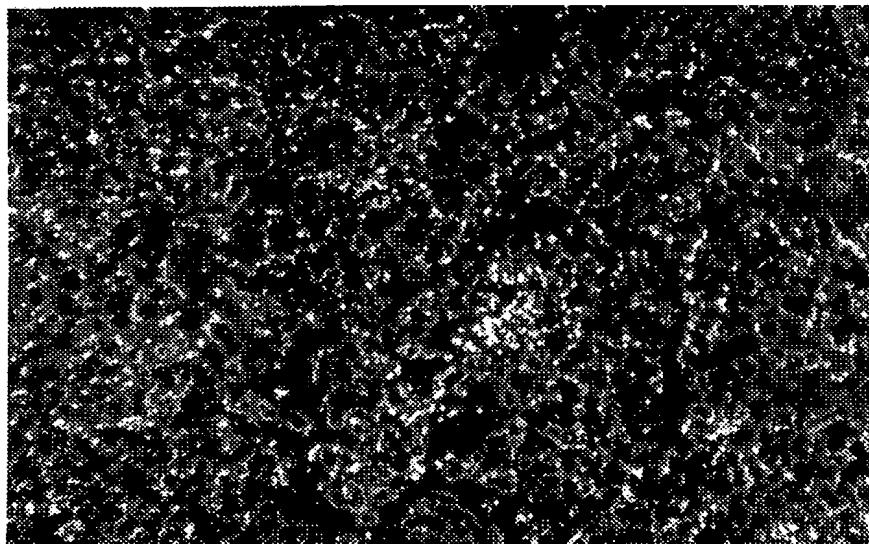
Darkfield

FIG. 20B



Lightfield

FIG.21A



Darkfield

FIG.21B